

# SEQ ID NO: 38

RESULT 7

AAV88429

ID AAV88429 standard; cDNA; 481 BP.

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AC AAV88429;

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DT 12-FEB-1999 (first entry)

XX

DE EST clone EM42.

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KW Expressed sequence tag; secreted protein; haematopoiesis regulator;

KW tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;

KW chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;

KW receptor; ligand; anti-inflammatory; tumour inhibitor; ds.

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OS Homo sapiens.

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PN US2002/0173635.

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PD 21 NOV 2002.

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PF 07 June 2002.

XX

PR 10-APR-1997; 97US-0837312.

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PA (GEMY ) GENETICS INST INC.

XX

PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;

PI Racie LA, Spaulding V, Treacy M;

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DR WPI; 1999-070078/06.

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PT New polynucleotides encoding human secreted proteins - derived from

PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,

PT ovary, pituitary, retina and colon cDNA libraries

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PS Claim 1; Page 394; 641pp; English.

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CC The present sequence represents an expressed sequence tag (EST), and is  
CC a polynucleotide of the invention. The polynucleotides of the invention  
CC are all secreted EST sequences isolated from a variety of human tissue  
CC sources. The EST sequences and proteins encoded by them are predicted to  
CC have useful biological activities which would make them suitable for  
CC treating, preventing or ameliorating medical conditions in humans and  
CC animals, although no supporting data is given. Suggested activities  
CC include nutritional activity, immune stimulating or suppressing activity,  
CC haematopoiesis regulating activity, tissue growth activity,  
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory  
CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition  
CC activity. The EST sequences are also stated to be useful for gene  
CC therapy.

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SQ Sequence 481 BP; 89 A; 127 C; 114 G; 151 T; 0 other;

Query Match 35.7%; Score 452.4; DB 20; Length 481;

Best Local Similarity 99.8%; Pred. No. 1.4e-102;

Matches 453; Conservative 0; Mismatches 1; Indels 0; Gaps

0;

Qy	484	AACTGGTGCTGGTTTCACATCACGACAGCAACGGGATTCTTTTGCTTTGAAAATGTTGCA	543
Db	22	AACTGGTGCTGGTTTCACATCACGACAGCAACGGGATTCTTTTGCTTTGAAAATGTTGCA	81
Qy	544	GTCCACCTGTCCAACTTGATCTTCCGGACATTTGACTTGTTTCTGGTTATCCACCATCTC	603
Db	82	GTCCACCTGTCCAACTTGATCTTCCGGACATTTGACTTGTTTCTGGTTATCCACCATCTC	141
Qy	604	TTTGCCTTTCTTGGGTTTCTTGGCTGCTTGGTCAATCTCCAAGCTGGCCACTATCTAGCT	663
Db	142	TTTGCCTTTCTTGGGTTTCTTGGCTGCTTGGTCAATCTCCAAGCTGGCCACTATCTAGCT	201
Qy	664	ATGACCACGTTGCTCCTGGAGATGAGCACGCCCTTTACCTGCGTTTCCTGGATGCTCTTA	723
Db	202	ATGACCACGTTGCTCCTGGAGATGAGCACGCCCTTTACCTGCGTTTCCTGGATGCTCTTA	261
Qy	724	AAGGCGGGCTGGTCCGAGTCTCTGTTTTGGAAGCTCAACCAGTGGCTGATGATTCACATG	783
Db	262	AAGGCGGGCTGGTCCGAGTCTCTGTTTTGGAAGCTCAACCAGTGGCTGATGATTCACATG	321
Qy	784	TTTCACTGCCGCATGGTTCTAACCTACCACATGTGGTGGGTGTGTTTCTGGCACTGGGAC	843
Db	322	TTTCACTGCCGCATGGTTCTAACCTACCACATGTGGTGGGTGTGTTTCTGGCACTGGGAC	381
Qy	844	GGCCTGGTCAGCAGCCTGTATCTGCCTCATTTGACACTGTTTCCTTGTCGGACTGGCTCTG	903
Db	382	GGCCTGGTCAGCAGCCTGTATCTGCCTCATTTGACACTGTTTCCTTGTCGGACTGGCTCTG	441
Qy	904	CTTACGCTAATCATTAATCCATATTGGACCCATA	937
Db	442	CTTACGCTAATCATTAATCCATATTGGACCCAGA	475